

Supplementary information S1 (table). Pathogen GWASs in NHGRI GWAS catalog (<https://www.genome.gov/26525384>) as of April 15, 2014

Disease or Pathogen	Reference	Pubmed ID	minimum observed p-value	# reported loci (# p<1×10 <sup>-8</sup> )	Study (title)	Phenotypes tested	GWAS sample set	Replication sample set
anthrax	Pajewski 2012	22658931	1E-06	8 (0)	A genome-wide association study of host genetic determinants of the antibody response to Anthrax Vaccine Adsorbed.	Immune response to anthrax vaccine	726 European ancestry individuals	
cytomegalovirus	Kuparinen 2011	21993531	8E-07	9 (0)	Genome-wide association study does not reveal major genetic determinants for anti-cytomegalovirus antibody response.	Cytomegalovirus antibody response	1,485 European ancestry sero-positive individuals, 648 European ancestry sero-negative individuals	
dengue shock syndrome	Khor 2011	22001756	4E-11	4 (2)	Genome-wide association study identifies susceptibility loci for dengue shock syndrome at MICB and PLCE1.	Dengue shock syndrome	2,008 Vietnamese ancestry cases, 2,018 Vietnamese ancestry controls	1,737 Vietnamese ancestry cases, 2,934 Vietnamese ancestry controls
Epstein-Barr virus	Rubicz 2013	23326239	3E-13	2 (2)	A genome-wide integrative genomic study localizes genetic factors influencing antibodies against Epstein-Barr virus nuclear antigen 1 (EBNA-1).	Epstein-Barr virus immune response (EBNA-1)	1,367 Mexican American individuals	589 Mexican American individuals
helicobacter pylori	Tanikawa 2012	22387998	2E-33	2 (2)	A genome-wide association study identifies two susceptibility loci for duodenal ulcer in the Japanese population.	Duodenal ulcer	1,043 Japanese ancestry cases, 21,694 Japanese ancestry controls	5,992 Japanese ancestry cases, 3,629 Japanese ancestry controls
helicobacter pylori	Mayerle 2013	23652523	1E-18	2 (1)	Identification of genetic loci associated with Helicobacter pylori serologic status.	Helicobacter pylori serologic status	2,623 European ancestry high titer cases, 7,862 European ancestry low or no titer controls	
hepatitis B	Mbarek 2011	21750111	2E-61	4 (4)	A genome-wide association study of chronic hepatitis B identified novel risk locus in a Japanese population.	Hepatitis B	458 Japanese ancestry cases, 2,056 Japanese ancestry controls	2,209 Japanese ancestry cases, 4,440 Japanese ancestry controls
hepatitis B	Nishida 2012	22737229	4E-45	2 (2)	Genome-wide association study confirming association of HLA-DP with protection against chronic hepatitis B and viral clearance in Japanese and Korean.	Hepatitis B (viral clearance)	181 East Asian ancestry HBV carriers, 184 East Asian ancestry controls, 185 East Asian ancestry spontaneously HBV-resolved individuals	Up to 8,045 East Asian ancestry HBV carriers, up to 9,003 East Asian ancestry controls, and up to 3,995 East Asian ancestry spontaneously HBV-resolved individuals
hepatitis B	Kim 2013	23760081	4E-40	6 (6)	A genome-wide association study identified new variants associated with the risk of chronic hepatitis B.	Chronic hepatitis B infection	400 Korean ancestry cases, 1,000 Korean ancestry controls	971 Korean ancestry cases, 1,938 Korean ancestry controls
hepatitis B	Kamatani 2009	19349983	6E-39	1 (1)	A genome-wide association study identifies variants in the HLA-DP locus associated with chronic hepatitis B in Asians.	Hepatitis B	179 Japanese ancestry cases, 934 Japanese ancestry controls	1,599 Japanese ancestry cases, 2,821 Japanese ancestry controls, 308 Thai ancestry cases, 546 Thai ancestry controls

hepatitis B	Hu 2013	24162738	5E-37	3 (3)	New loci associated with chronic hepatitis B virus infection in Han Chinese.	Hepatitis B	951 Han Chinese HBV carrier cases, 937 Han Chinese HBV cleared controls	4,230 Chinese ancestry HBV carrier cases, 3,051 Chinese ancestry HBV cleared controls, 2,622 Chinese ancestry controls
hepatitis B	Li 2012	22807686	5E-22	3 (2)	GWAS identifies novel susceptibility loci on 6p21.32 and 21q21.3 for hepatocellular carcinoma in chronic hepatitis B virus carriers.	Hepatocellular carcinoma	1,538 Han Chinese HBV-positive HCC cases, 1,465 Han Chinese chronic HBV carriers	4,431 Han Chinese HBV-positive HCC cases, 4,725 Han Chinese chronic HBV carriers
hepatitis B	Png 2011	21764829	7E-22	3 (3)	A genome-wide association study of hepatitis B vaccine response in an Indonesian population reveals multiple independent risk variants in the HLA region.	Hepatitis B vaccine response	1,683 Indonesian ancestry individuals	1,931 Indonesian ancestry individuals
hepatitis B	Zhang 2010	20676096	2E-18	1 (1)	Genome-wide association study identifies 1p36.22 as a new susceptibility locus for hepatocellular carcinoma in chronic hepatitis B virus carriers.	Hepatocellular carcinoma	348 Chinese ancestry cases, 359 Chinese ancestry controls	1,962 Chinese ancestry cases, 1,430 Chinese ancestry controls, 159 Chinese ancestry trios
hepatitis B	Jiang 2012	23242368	3E-17	2 (2)	Genetic variants in STAT4 and HLA-DQ genes confer risk of hepatitis B virus-related hepatocellular carcinoma.	Hepatocellular carcinoma (hepatitis B virus related)	1,161 Chinese ancestry cases, 1,353 Chinese ancestry controls	4,319 Chinese ancestry cases, 4,966 Chinese ancestry controls
hepatitis B	Liu 2011	22004137	2E-08	1 (0)	A genome-wide association study with DNA pooling identifies the variant rs11866328 in the GRIN2A gene that affects disease progression of chronic HBV infection.	Hepatitis B	1944 Chinese ancestry cases, 854 Chinese ancestry controls	
hepatitis B	Chan 2011	22174901		0 (0)	Genome-wide association study of hepatocellular carcinoma in Southern Chinese patients with chronic hepatitis B virus infection.	Hepatocellular carcinoma	95 Chinese ancestry cases, 97 Chinese ancestry controls.	500 Chinese ancestry cases, 728 Chinese ancestry controls.
hepatitis B	Al-Qahtani 2013	24065354		0 (0)	Genome-wide association study of chronic hepatitis B virus infection reveals a novel candidate risk allele on 11q22.3.	Liver disease in chronic hepatitis B virus infection	up to 305 Arab ancestry cases, 343 Arab ancestry controls	48 Arab ancestry cases, 177 Arab ancestry controls
hepatitis C	Fellay 2010	20173735	9E-76	2 (2)	ITPA gene variants protect against anaemia in patients treated for chronic hepatitis C.	Chronic Hepatitis C infection	988 European-American cases, 198 African-American cases, 100 Hispanic cases	
hepatitis C	Tanaka 2009	19749757	3E-32	1 (1)	Genome-wide association of IL28B with response to pegylated interferon-alpha and ribavirin therapy for chronic hepatitis C.	Response to hepatitis C treatment	72 Japanese responders, 82 Japanese non-responders	122 Japanese responders, 50 Japanese non-responders
hepatitis C	Ge 2009	19684573	1E-28	3 (1)	Genetic variation in IL28B predicts hepatitis C treatment-induced viral clearance.	Response to hepatitis C treatment	871 European ancestry, 191 African American, and 75 Hispanic ancestry individuals	
hepatitis C	Tanaka 2011	21659334	2E-25	2 (2)	Genome-wide association study identified ITPA/DDRKG1 variants reflecting thrombocytopenia in pegylated interferon and ribavirin therapy for chronic hepatitis C.	Response to hepatitis C treatment	303 Japanese ancestry cases	391 Japanese ancestry cases

hepatitis C	Ochi 2011	21228123	1E-20	1 (1)	IL-28B predicts response to chronic hepatitis C therapy--fine-mapping and replication study in Asian populations.	Response to hepatitis C treatment	2,028 Japanese cases, 73 Taiwanese cases, 282 Japanese controls	
hepatitis C	Clark 2012	22497812	5E-17	1 (1)	Interleukin 28B polymorphisms are the only common genetic variants associated with low-density lipoprotein cholesterol (LDL-C) in genotype-1 chronic hepatitis C and determine the association between LDL-C and treatment response.	Lipid levels in hepatitis C treatment	1,017 European ancestry cases, 207 African American ancestry cases, 95 Hispanic cases	
hepatitis C	Miki 2011	21725309	1E-13	1 (1)	Variation in the DEPDC5 locus is associated with progression to hepatocellular carcinoma in chronic hepatitis C virus carriers.	Chronic Hepatitis C infection	212 Japanese ancestry cases, 765 Japanese ancestry controls	710 Japanese ancestry cases, 1,625 Japanese ancestry controls
hepatitis C	Kumar 2011	21499248	4E-13	2 (2)	Genome-wide association study identifies a susceptibility locus for HCV-induced hepatocellular carcinoma.	Hepatocellular carcinoma	721 Japanese ancestry cases, 2,890 Japanese ancestry controls	673 Japanese ancestry cases, 2,596 Japanese ancestry controls
hepatitis C	Urabe 2013	23321320	9E-11	5 (5)	A genome-wide association study of HCV-induced liver cirrhosis in the Japanese population identifies novel susceptibility loci at the MHC region.	Hepatitis C induced liver cirrhosis	682 Japanese ancestry cases, 1,045 Japanese ancestry controls	936 Japanese ancestry cases, 3,809 Japanese ancestry controls
hepatitis C	Thompson 2011	21703177	1E-09	1 (1)	Genome-wide association study of interferon-related cytopenia in chronic hepatitis C patients.	IFN-related cytopenia	984 European ancestry with genotype 1 HCV, 201 African Americans ancestry with genotype 1 HCV, 99 Hispanics ancestry with genotype 1 HCV	
hepatitis C	Patin 2012	22841784	1E-09	6 (2)	Genome-wide association study identifies variants associated with progression of liver fibrosis from HCV infection.	Hepatitis C induced liver fibrosis	1,161 European ancestry HCV-infected individuals	1,181 European ancestry HCV-infected individuals
hepatitis C	Rauch 2010	20060832	6E-09	1 (1)	Genetic variation in IL28B is associated with chronic hepatitis C and treatment failure: a genome-wide association study.	Chronic Hepatitis C infection	1,015 Swiss chronic HCV patients, 347 Swiss spontaneously cleared HCV patients	
hepatitis C	Suppiah 2009	19749758	9E-09	1 (1)	IL28B is associated with response to chronic hepatitis C interferon-alpha and ribavirin therapy.	Response to hepatitis C treatment	131 European ancestry responders, 162 European ancestry non-responders	261 European responders, 294 European non-responders
hepatitis C	Lange 2011	22095909	1E-06	9 (0)	Serum ferritin levels are associated with a distinct phenotype of chronic hepatitis C poorly responding to pegylated interferon-alpha and ribavirin therapy.	Response to hepatitis C treatment	707 European ancestry cases	
hepatitis C	Duggal 2013	23420232		0 (0)	Genome-wide association study of spontaneous resolution of hepatitis C virus infection: data from multiple cohorts.	Chronic Hepatitis C infection	1,482 chronic HCV patients, 919 spontaneously cleared HCV patients	461 chronic HCV patients, 284 spontaneously cleared HCV patients

HIV	Pereyra 2010	21051598	3E-35	8 (8)	The major genetic determinants of HIV-1 control affect HLA class I peptide presentation.	HIV-1 control	516 European cases, 1,196 European controls, 341 African American cases, 892 African American controls, 117 Hispanic controls, 560 Hispanic controls	
HIV	Fellay 2009	20041166	5E-35	40 (2)	Common genetic variation and the control of HIV-1 in humans.	HIV-1 control	2,362 Caucasian cases	
HIV	Limou 2009	19115949	3E-19	3 (1)	Genomewide association study of an AIDS-nonprogression cohort emphasizes the role played by HLA genes (ANRS Genomewide Association Study 02).	AIDS progression	275 HIV positive patients, 1,438 controls	626 patients
HIV	McLaren 2013	23935489	4E-11	1 (1)	Association study of common genetic variants and HIV-1 acquisition in 6,300 infected cases and 7,200 controls.	HIV-1 susceptibility	6,334 European ancestry cases, 7,247 European ancestry controls	
HIV	Troyer 2011	21502085	3E-09	7 (1)	Genome-wide association study implicates PARD3B-based AIDS restriction.	AIDS progression	755 European ancestry seroconverters	
HIV	Shrestha 2010	20009918	3E-08	7 (0)	A genome-wide association study of carotid atherosclerosis in HIV-infected men.	Carotid atherosclerosis in HIV infection	177 Caucasian HIV-infected men	
HIV	Levine 2012	22628157	1E-07	4 (0)	Genome-wide association study of neurocognitive impairment and dementia in HIV-infected adults.	HIV-associated dementia	1,287 European ancestry HIV-infected men	
HIV	Lingappa 2011	22174851	2E-07	23 (0)	Genomewide association study for determinants of HIV-1 acquisition and viral set point in HIV-1 serodiscordant couples with quantified virus exposure.	HIV-1 susceptibility; HIV-1 viral setpoint	798 African ancestry individuals	
HIV	Le 2009	19754311	6E-07	7 (0)	Genomewide association study of a rapid progression cohort identifies new susceptibility alleles for AIDS (ANRS Genomewide Association Study 03).	AIDS	85 French cases, 2,049 French controls	
HIV	Pelak 2010	20205591	1E-06	10 (0)	Host determinants of HIV-1 control in African Americans.	HIV-1 control	515 African American cases	
HIV	Petrovski 2010	21160409	4E-06	6 (0)	Common human genetic variants and HIV-1 susceptibility: a genome-wide survey in a homogeneous African population.	HIV-1 susceptibility	848 Malawian cases, 531 Malawian controls	
HIV	Bol 2011	21364930	5E-06	1 (0)	Genome-wide association study identifies single nucleotide polymorphism in DYRK1A associated with replication of HIV-1 in monocyte-derived macrophages.	HIV-1 replication	191 European ancestry individuals	31 individuals
HIV	Fellay 2007	17641165		0 (0)	A whole-genome association study of major determinants for host control of HIV-1.	HIV-1 viral setpoint	486 patients	140 patients

HIV	Joubert 2010	20487506		0 (0)	A whole genome association study of mother-to-child transmission of HIV in Malawi.	HIV (mother-to-child transmission)	100 Malawian infant cases, 126 Malawian infant controls	
HIV	van 2011	21811574		0 (0)	Genome-wide association scan in HIV-1-infected individuals identifying variants influencing disease course.	HIV-1 progression	404 cases	
HIV	Lane 2013	23372042		0 (0)	A genome-wide association study of resistance to HIV infection in highly exposed uninfected individuals with hemophilia A.	HIV-1 susceptibility	430 exposed uninfected Haemophilia cases, 765 HIV positive controls	
human papillomavirus	Chen 2011	21896673	1E-14	1 (1)	Genome-wide association study of HPV seropositivity.	HPV seropositivity	1,286 European ancestry lung cancer cases, 679 European ancestry head and neck cancer cases, 811 European ancestry kidney cancer cases, 2,035 European ancestry controls	1,307 European and Hispanic head and neck cancer cases, 1,037 European and Hispanic controls
influenza	Zhou 2012	22693232		0 (0)	A functional variation in CD55 increases the severity of 2009 pandemic H1N1 influenza A virus infection.	Influenza (severity)	25 Chinese ancestry severe cases, 26 Chinese ancestry controls	152 Chinese ancestry severe cases, 222 Chinese ancestry controls
leishmaniasis	LeishGEN 2013	23291585	3E-17	1 (1)	Common variants in the HLA-DRB1-HLA-DQA1 HLA class II region are associated with susceptibility to visceral leishmaniasis.	Leishmaniasis (visceral)	889 Indian ancestry cases, 977 Indian ancestry controls, 357 Brazilian ancestry cases, and 1,615 Brazilian ancestry unaffected relatives	889 Indian ancestry cases, 948 Indian ancestry controls.
Leprosy	Zhang 2009	20018961	4E-54	6 (6)	Genomewide association study of leprosy.	Leprosy	706 Han Chinese cases, 1,225 Han Chinese controls	3,254 Chinese cases, 5,955 Chinese controls
Leprosy	Zhang 2011	22019778	4E-14	4 (3)	Identification of two new loci at IL23R and RAB32 that influence susceptibility to leprosy.	Leprosy	706 Chinese ancestry cases, 5,581 Chinese ancestry controls	3,301 Chinese ancestry cases, 5,299 Chinese ancestry controls
malaria	Timmann 2012	22895189	4E-21	4 (3)	Genome-wide association study indicates two novel resistance loci for severe malaria.	Malaria	1,325 African ancestry, 828 African ancestry controls	2,229 African ancestry cases, 3,526 African ancestry controls
malaria	Band 2013	23717212	2E-16	6 (2)	Imputation-based meta-analysis of severe malaria in three African populations.	Malaria	5,425 African cases, 6,891 African controls	
malaria	Jallow 2009	19465909	4E-11	3 (1)	Genome-wide and fine-resolution association analysis of malaria in West Africa.	Malaria	958 African ancestry cases, 1,382 African ancestry controls, all children	1,087 African ancestry cases, 2,376 African ancestry controls, all children
meningococcal disease	Davila 2010	20694013	5E-13	1 (1)	Genome-wide association study identifies variants in the CFH region associated with host susceptibility to meningococcal disease.	Meningococcal disease	475 UK Caucasian cases, 4,703 UK controls	514 Western European cases, 814 Western European controls, 415 Spanish cases, 537 Spanish controls
prion diseases	Mead 2008	19081515	2E-21	2 (1)	Genetic risk factors for variant Creutzfeldt-Jakob disease: a genome-wide association study.	Creutzfeldt-Jakob disease	117 CJD cases, 3,083 controls	506 sCJD cases, 28 iCJD cases, 151 Kuru cases, 125 Kuru-resistant cases, up to 1,137 controls

prion diseases	Sanchez-Juan 2011	22137330	3E-18	6 (1)	Genome-wide study links MTMR7 gene to variant Creutzfeldt-Jakob risk.	Creutzfeldt-Jakob disease (variant)	93 European ancestry cases, 1,504 European ancestry controls	42 European ancestry cases
prion diseases	Mead 2011	22210626	7E-07	11 (0)	Genome-wide association study in multiple human prion diseases suggests genetic risk factors additional to PRNP.	Prion diseases	1,281 European ancestry cases, 6,015 European ancestry controls, 290 Papua New Guinea cases, 286 Papua New Guinea controls.	
smallpox	Kennedy 2012	22610502	2E-18	93 (32)	Genome-wide analysis of polymorphisms associated with cytokine responses in smallpox vaccine recipients.	IL-2; IL-6; IL-10; IL-12p40; IL-1beta; TNF-alpha; IFN-alpha	Up to 512 European ancestry individuals, 199 African American individuals	
smallpox	Ovsyannikova 2012	22542470	1E-10	37 (5)	Genome-wide association study of antibody response to smallpox vaccine.	Immune response to smallpox vaccine (IL-6)	217 African American ancestry individuals, 580 European ancestry individuals, 217 Hispanic ancestry individuals	
tuberculosis	Chimusa 2013	24057671	1E-12	27 (2)	Genome-wide association study of ancestry-specific TB risk in the South African Coloured population.	Tuberculosis	642 South African coloured cases, 91 South African coloured controls	
tuberculosis	Thye 2012	22306650	3E-11	1 (1)	Common variants at 11p13 are associated with susceptibility to tuberculosis.	Tuberculosis	1,329 African ancestry cases, 1,847 African ancestry controls	2,024 African ancestry cases, 5,154 African ancestry controls, 1,025 Indonesian ancestry cases, 983 Indonesian ancestry controls, 4,441 European ancestry cases, 5,874 European ancestry controls
tuberculosis	Thye 2010	20694014	7E-09	14 (1)	Genome-wide association analyses identifies a susceptibility locus for tuberculosis on chromosome 18q11.2.	Tuberculosis	921 Ghanaian cases 1,740 Ghanaian controls, 1,316 Gambian cases, 1,382 Gambian controls	1,226 Ghanaian cases, 3,825 Ghanaian controls, 236 Malawian cases, 779 Malawian controls, 332 Ghana parent/child trios and duos
tuberculosis	Png 2012	22239941		0 (0)	A genome wide association study of pulmonary tuberculosis susceptibility in Indonesians.	Tuberculosis	108 Indonesian ancestry cases, 115 Indonesian ancestry controls	600 Indonesian ancestry cases, 540 Indonesian ancestry controls, 1,837 European ancestry cases, 1,779 European ancestry controls
tuberculosis	Mahasirimongkol 2012	22551897		0 (0)	Genome-wide association studies of tuberculosis in Asians identify distinct at-risk locus for young tuberculosis.	Tuberculosis	433 Thai ancestry cases, 295 Thai ancestry controls, 188 Japanese ancestry cases, 934 Japanese ancestry controls	369 Thai ancestry cases, 439 Thai ancestry controls, 112 Japanese ancestry cases, 1,089 Japanese ancestry controls